

FIG. 1

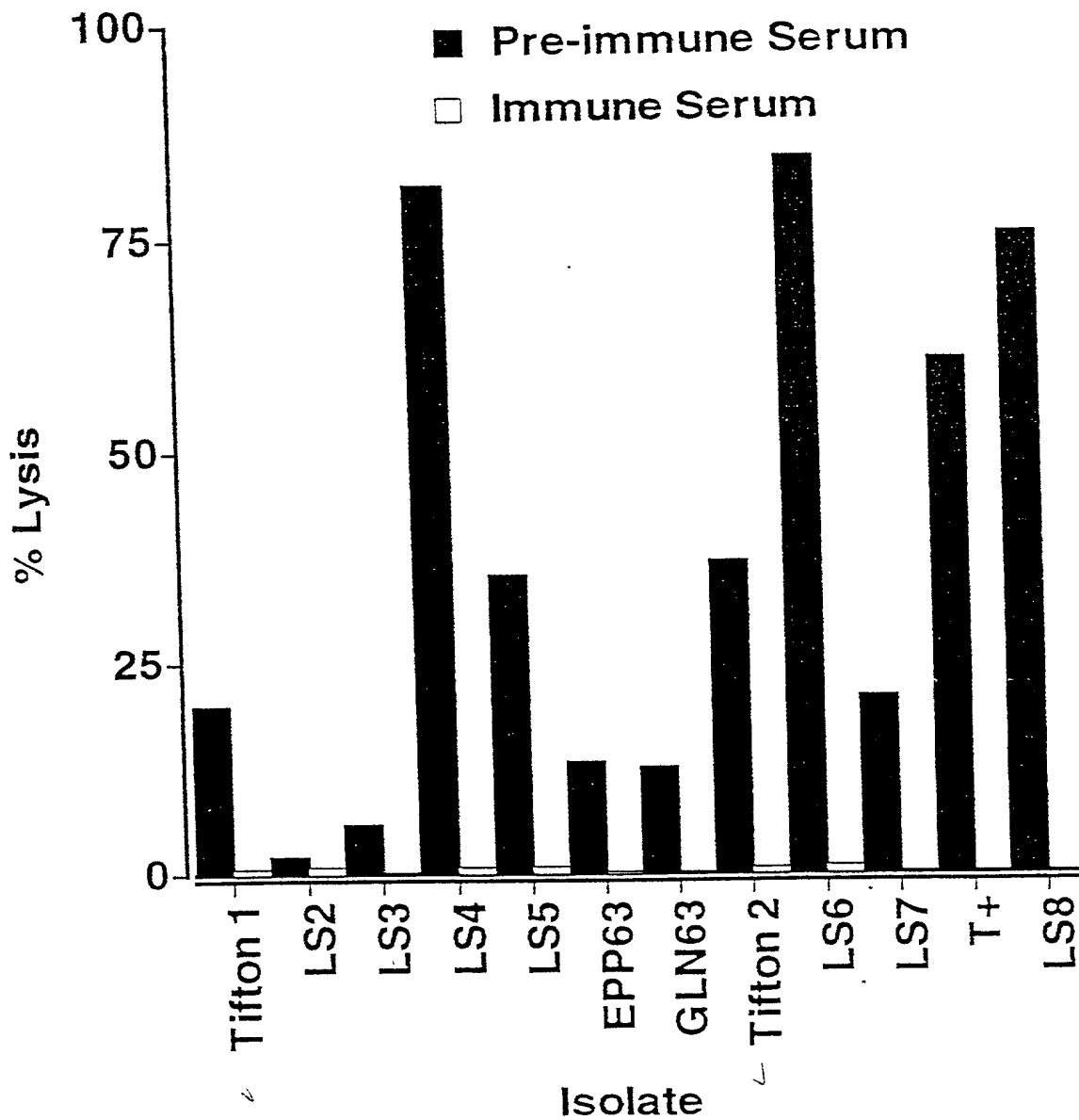


FIG. 2

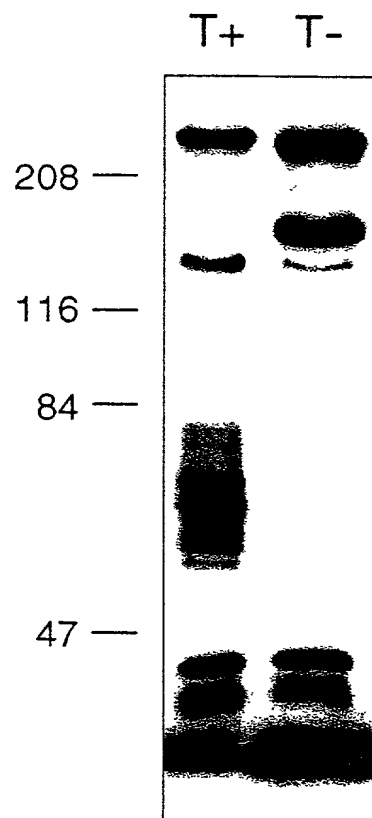


FIG 3-1

Appendix A update-July 1999

Bases 1-1200

Amino acids 1-400

1	ATGTCCAATATAAATGTAATTAAATCTAATATTCAAGCAGGCTTGAATTCAACAAAGTCT	60
1	M S N I N V I K S N I Q A G L N S T K S	20
61	GGATTAAAAAATCTTTACTTGGCTATTCCCAAAGATTATGATCCGCAAAAAGGTGGGACT	120
21	G L K N L Y L A I P K D Y D P Q K G G T	40
121	TTAAATGATTTTATTAAAGCTGCTGATGAATTAGGTATTGCTCGTTTAGCAGAAGAGCCT	180
41	L N D F I K A A D E L G I A R L A E E P	60
181	AATCACACTGAAACAGCAAAAAAATCTGTTGACACAGTAAATCAGTTTCTCTCTCTCACA	240
61	N H T E T A K K S V D T V N Q F L S L T	80
241	CAAACGGTATTGCTATTTCTGCAACAAAATTAGAAAAGTTCTTACAAAAACATTCTACC	300
81	Q T G I A I S A T K L E K F L Q K H S T	100
301	AATAAGTTAGCCAAAGGGTTAGACAGTGTAGAAAATATTGATCGTAAATTAGGTAAAGCA	360
101	N K L A K G L D S V E N I D R K L G K A	120
361	AGTAATGTATTATCAACATTAAGCTCTTTTTTGGGCACTGCATTAGCGGGTATAGAAGCTT	420
121	S N V L S T L S S F L G T A L A G I E L	140
421	GATTCCTTAATCAAAAAAGGTGATGCTGCACCTGATGCTTTGGCTAAAGCTAGTATTGAC	480
141	D S L I K K G D A A P D A L A K A S I D	160
481	TTGATTAATGAGATAATTGGTAATCTATCTCAGAGTACTCAAACGATTGAAGCATTTTCT	540
161	L I N E I I G N L S Q S T Q T I E A F S	180
541	TCACAGTTAGCAAAGTTAGGTTCTACTATATCGCAGGCTAAAGGCTTCTCTAATATAGGA	600
181	S Q L A K L G S T I S Q A K G F S N I G	200
601	AACAAGTTGCAAACTTAAATTTTTCTAAAACAAATCTTGGTTTGGAAATAATTACTGGT	660
201	N K L Q N L N F S K T N L G L E I I T G	220
661	TTGCTATCAGGCATTTCTGCAGGCTTTGCTTTAGCGGATAAAAAATGCATCGACTGGCAAA	720
221	L L S G I S A G F A L A D K N A S T G K	240
721	AAAGTTGCTGCAGGTTTTGAATTAAGCAATCAAGTTATTGGTAATGTAACAAAGCAATT	780
241	K V A A G F E L S N Q V I G N V T K A I	260
781	TCTTCATATGTTTTAGCACACGTGTTGCTGCTGGTCTATCAACTACTGGTGCTGTTGCT	840
261	S S Y V L A Q R V A A G L S T T G A V A	280
841	GCTTTAATTACTTCATCGATTATGTTGGCAATTAGTCCTTTGGCATTATGAATGCAGCA	900
281	A L I T S S I M L A I S P L A F M N A A	300
901	GATAAATTCAATCATGCTAATGCTCTTGATGAGTTTGCAAAACAATTCCGAAAATTTGGC	960
301	D K F N H A N A L D E F A K Q F R K F G	320
961	TATGATGGGGATCATTTATTGGCTGAATATCAGCGTGGTGTGGGTACTATTGAAGCTTCA	1020
321	Y D G D H L L A E Y Q R G V G T I E A S	340
1021	TTAACTACAATTAGTACGGCATTAGGTGCAGTTTCTGCTGGTGTTCGCTGCTGCTGTA	1080
341	L T T I S T A L G A V S A G V S A A A V	360
1081	GGATCTGCTGTTGGTGCACCGATTGCACTATTAGTTGCAGGTGTTACAGGATTGATCTCT	1140
361	G S A V G A P I A L L V A G V T G L I S	380
1141	GGAATTTTAGAAGCGTCTAAACAGGCAATGTTTGAAAGTGTTGCTAACCGTTTACAAGGT	1200
381	G I L E A S K Q A M F E S V A N R L Q G	400

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FIG 3-2

Appendix A update-July 1999, continued

Bases 1201-2400

Amino acids 401-800

1201	AAAATTTTAGAGTGGGAAAAGCAAAATGGCGGTCAGAACTATTTTGATAAAGGCTATGAT	1260
401	K I L E W E K Q N G G Q N Y F D K G Y D	420
1261	TCTCGTTATGCTGCTTATTTAGCTAATAACTTAAAATTTTGTCTGAGCTAAATAAGAG	1320
421	S R Y A A Y L A N N L K F L S E L N K E	440
1321	TTGGAAGCTGAACGTGTTATTGCAATCACCCAACAACGTTGGGATAATAATATTGGTGAG	1380
441	L E A E R V I A I T Q Q R W D N N I G E	460
1381	TTAGCAGGTATTACCAAATTGGGTGAACGCATTAAGAGCGGAAAAGCTTATGCAGATGCT	1440
461	L A G I T K L G E R I K S G K A Y A D A	480
1441	TTTGAAGATGGCAAGAAAGTTGAAGCTGGTTCCAATATTACTTTGGATGCTAAAAGCTGGT	1500
481	F E D G K K V E A G S N I T L D A K T G	500
1501	ATCATAGACATTAGTAATTCAAATGGGAAAAAACGCAAGCGTTGCATTTCACTTCGCCT	1560
501	I I D I S N S N G K K T Q A L H F T S P	520
1561	TTGTTAACAGCAGGAAGTGAATCACGTGAACGTTTAACTAATGGTAAATACTCTTATATT	1620
521	L L T A G T E S R E R L T N G K Y S Y I	540
1621	AATAAGTTAAAATTCGGACGTGTAAAAAACTGGCAAGTTACAGATGGAGAGGCTAGTTCT	1680
541	N K L K F G R V K N W Q V T D G E A S S	560
1681	AAATTAGATTTCTCTAAAGTTATTCAGCGTGTAGCCGAGACAGAAGGCACAGACGAGATT	1740
561	K L D F S K V I Q R V A E T E G T D E I	580
1741	GGTCTAATAGTAAATGCAAAAGCTGGCAATGACGATATCTTTGTTGGTCAAGGTAAAATG	1800
581	G L I V N A K A G N D D I F V G Q G K M	600
1801	AATATTGATGGTGGAGATGGACACGATCGTGTCTTCTATAGTAAAGACGGAGGATTTGGT	1860
601	N I D G G D G H D R V F Y S K D G G F G	620
1861	AATATTACTGTAGATGGTACGAGTGCAACAGAAGCAGGCAGTTATACAGTTAATCGTAAG	1920
621	N I T V D G T S A T E A G S Y T V N R K	640
1921	GTTGCTCGAGGTGATATCTACCATGAAGTTGTGAAGCGTCAAGAAACCAAGGTGGGTAAA	1980
641	V A R G D I Y H E V V K R Q E T K V G K	660
1981	CGTACTGAAACTATCCAGTATCGTGATTATGAATTAAGAAAAGTTGGGTATGGTTATCAG	2040
661	R T E T I Q Y R D Y E L R K V G Y G Y Q	680
2041	TCTACCGATAATTTGAAATCAGTAGAAGAAGTAATTGGTTCTCAATTTAATGATGTATTTC	2100
681	S T D N L K S V E E V I G S Q F N D V F	700
2101	AAAGGTTCTAAATTCAACGACATATTCATAGTGGTGAAGGTGATGATTTACTCGATGGT	2160
701	K G S K F N D I F H S G E G D D L L D G	720
2161	GGTGCTGGTGACGACCGCTTGTGGTGGTAAAGGCAACGATCGACTTTCTGGAGATGAA	2220
721	G A G D D R L F G G K G N D R L S G D E	740
2221	GGCGATGATTTACTCGATGGCGGTTCTGGTGATGATGTATTAATGGTGGTGCTGGTAAT	2280
741	G D D L L D G G S G D D V L N G G A G N	760
2281	GATGTCTATATCTTTGAAAGGTGATGGTAATGATACTTTGTACGATGGCACGGGCAAT	2340
761	D V Y I F R K G D G N D T L Y D G T G N	780
2341	GATAAATTAGCATTTGCAGATGCAAAATATATCTGATATTATGATTGAACGTACCAAAGAG	2400
781	D K L A F A D A N I S D I M I E R T K E	800

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FIG 3-3

Appendix A update-July 1999, continued

Bases 2401-2784

Amino acids 801-927

2401	GGTATTATAGTTAAACGAAATGATCATTGAGGTAGTATTAACATACCAAGATGGTACATA	2460
801	G I I V K R N D H S G S I N I P R W Y I	820
2461	ACATCAAATTTACAAAATTATCAAAGTAATAAACAGATCATAAAATTGAGCAACTAATT	2520
821	T S N L Q N Y Q S N K T D H K I E Q L I	840
2521	GGTAAAGATGGTAGTTATATCACTTCCGATCAAATTGATAAAATTTTGCAAGATAAGAAA	2580
841	G K D G S Y I T S D Q I D K I L Q D K K	860
2581	GATGGTACAGTAATTACATCTCAAGAATTGAAAAAGCTTGCTGATGAGAATAAGAGCCAA	2640
861	D G T V I T S Q E L K K L A D E N K S Q	880
2641	AAATTATCTGCTTCGGACATTGCAAGTAGCTTAAATAAGCTAGTTGGGTCAATGGCACTA	2700
881	K L S A S D I A S S L N K L V G S M A L	900
2701	TTTGGTACAGCAAATAGTGTGAGTTCTAACGCCTTACAGCCAATTACACAACCAACTCAA	2760
901	F G T A N S V S S N A L Q P I T Q P T Q	920
2761	GGAATTTTGGCTCCAAGTGTTTAG	2784
921	G I L A P S V *	928

SEQ ID NO: 1
SEQ ID NO: 2

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[illegible]

MbxA	LkxA	- M G T T R L T T T L S	- N G L K N K T T T T A T	- S G L K N Q M S N I N	V I K S N I T Q A G L	N T S L S G A K N L Z	Y L A T P K N Y D V Y	D P Q K G	38
ApixIIA	HlyA	M S P T T T A A Q L K	S T L Q Q S A K Q S A	A N K L N Q A G Q T S	L K N G L T Q A G L	H S L Q N Q A K N L Z	I L L T P Q Q G . . .	D S Q G G	59
						Q T R N A G A N L	I L L T P K D Y K . .	G O G	62
								G O G	61
MbxA	LkxA	G T L N D F K A A	D E L G I A R L A	E P N H T E T A K K	S V D T T V N Q F L S	L T T T G A T S A	T K L K F L Q K H	S T N K L	103
ApixIIA	HlyA	N G L V Q Q D L V K A A	N L G I E V O V R E	E R S N I I A T A Q T	S L G D T T Q T A I L G	L T T T G A T S A	F O L D K L L Q K .	T N K A	121
		S S L N D L V L T A	D E L G I E V O V Y	E N G T A I T K T	V F G T T A K L I G	L T T T G A T S A	F O L D K L L Q K .	N P K A	125
							F O L D K L L Q K Y	Q . . K A	124
MbxA	LkxA	A Q G L L D S A E N	I D R K L A N K A S N	V L S T T Q S S I L G	T A L A G I E L D S	L I K K G D	A A P D A L A K A G	I L T I N	163
ApixIIA	HlyA	G N K L L G S A S S	I G D N L G R A N K S	V L G S T Q S S I L G	S V L A G G V N L N E R	L I K K K D	S P N Q L E L A K A G	I L E T I N	180
							V S S E L A K A G	I E L I N	185
									189
MbxA	LkxA	E I G N T S Q S T	O T L A F S S Q L I	A K L G S T T S O A	K G F S N T G N K L	O N L N F S K T N	L G L I I T G L L	S G I S A	227
ApixIIA	HlyA	S L V G N I A S S V	O T L D V E F G S Q L I	S O F G S K H L Q N V T	K G L G G T L G D K L	O N L G L D K A G	L G L D I S G L L	S G A T A	245
		L V D T A A S L	N N V N S F S Q L I	N K L O S V L Q N V T	K H L N G V G N K L	O N L P L D L N I G	A G L D T A S G L L	S A I S A	250
									253
MbxA	LkxA	G F A L A D K N A S	T G K K V G A G G F	L S H Q V I G N V T	K A V S S Y I L A Q	R V A A G L S T G C	A V A A L I A S T S	M L A I S	292
ApixIIA	HlyA	S F L T L S N A D A D	T G K K A A A G G F	P A N Q V G N V T	K A V S S Y I L A Q	R V A A G L S T G C	A V A A L I A S T S	A L A I S	310
									315
									318
MbxA	LkxA	L A F N A A D R	F N K A N A L E T	A K Q F K N F G Y D	G D H L L A E Y Q Q R	G V F G T T A A L L	T S T A L G A V S	A G V S A	357
ApixIIA	HlyA	P L A F A G I A D R	F N K Q A D L I K S	A A S R F F K N L G Y D	G D N R L L A G Y F H	F R G G T T A A L L	T S T A L A A I V S	G C V S A	375
		P L S L S V A D R	F K R A N K I E	S F K K L G Y D	G D S L L A A F H	F R G G T T A A L L	T S S V L A V S	S G S A	380
									383
MbxA	LkxA	A A V G S A V G A P	I A L L V A G V T G	V I S G I L E A S K	Q A M F E S V A N K	L O G K T I L E W E K	N N G G Q N Y F E K	G Y D S R	422
ApixIIA	HlyA	A A T T S L V G A P	V S A L V A G V T G	V I S G I L E A S K	Q A M F E S V A N K	L O G K T I L E W E K	N N G G Q N Y F E K	G Y D S R	440
									444
									447
MbxA	LkxA	Y A Y I A N N K	F L S E L N K K E L	A E R V I A I T Q Q	R W D N N I G E D L A	G H T T L G E F L K	S C K A Y A D A F E	G C K K V	487
ApixIIA	HlyA	H A D L O D N F K	F L S E L N K K E L	V E S V V A I T Q Q	H W D N N I G E D L A	G H T T L G E F L K	S C K A Y A D A F E	E G O H	505
									509
									512
MbxA	LkxA	E G S N T	T L D A K T G T T D	T S S S G G K K T O	A H F T S P L L T T	A G T S S R R R R T Q	N K K S T T N K L	K F G R V	548
ApixIIA	HlyA	S T D K L V	Q L D N K A N G I H N	T S S S G G K K T O	S V L F R T T P L L T	F G C E S R R R R R T Q	G C K S S T T N K L	H I O R V	569
		K K F P D Z F Q K Q	V F D P L K G N F D	L S S S . . K S S T	L K K F V T T P L L T	F G C E S R R R R R T Q	S O K Y K T I T E L	L L K G V	575
MbxA	LkxA	K N Q V T D . G	A S S K L D F S K V	I O R A G T E L D T	E G . . . T D E I	G Y H V A K A G A G	D D V V G Q G K M	N I D G G	605
ApixIIA	HlyA	D S W K T D . G A	A S S T F D L T N V	V O R A G T E L D T	A G N V T K T T E I	K H I A N L G A G A G	D D V V G S G T T	N I D G G	630
		D S W T V K G V Q D	K G S V Y D F T N L	I O R A S V K F D T	A G N I I Y E I	F H S H L G D G D	D D V V G S S T A	N I Y A G	633
									634
MbxA	LkxA	D G D R V F Y S K	D G G G N T T D	G S A T E A G S Y	T V N R K V . A R G	D I Y H V V R R Q	E K V G K R T E T	I Q Y R D	669
ApixIIA	HlyA	D G D R V F Y S R	G N Y G A L T I D	A T A T E K G S Y	T V N R F V . E T G	K A L E R V V R R Q	T A L V G N R E R	I E Y R .	692
		K G D R V F Y D K	T D T G Y L T T Y	G T A T E A G N Y	S V K R Y V . G D S	K A L E R V V R R Q	E V S V G K R T E K	T Q Y R S	695
									698
MbxA	LkxA	Y E L R K V . G Y G	Y Y T T D N L K S V	E E I G T S O F N D	I F K G S K F N D I A	F H S G G D G D L T	D G G A G D D L F	G G K G N	733
ApixIIA	HlyA	R E D D R F . H T G	Y Y T V T D S L K S V	E E I G T S O F N D	I F K G S K F N D I A	F H S G G D G D L T	D G G A G D D L F	G G K G N	756
		Y E F T H I N G K N	L T E T D N L Y S V	E E I G T T R A D	K F F G S K F N D I A	F H S G G D G D L T	D G G A G D D L F	G D K G N	759
									763
MbxA	LkxA	D I L D G G G D D	742
ApixIIA	HlyA	D I L D G G G D D	765
		D I L D G G G D D	Q L Y G G D G N D K	L T G A G N N Y L	N G G D G D D E L Q	V Q G N S L A K N V	L S G G K G N D K L	Y G S E G	768
									828
MbxA	LkxA	D I L D G G G D D	D V L L H G G A G N D	I Y F R K G D G N	D T I Y D G D T G . N	D K L S A F A D D A N L	S D M H E R T M E	G Y I T K	805
ApixIIA	HlyA	D I L D G G G D D	D V L L H G G A G N D	I Y F R K G D G N	D T I Y D G D T G . N	D K L S A F A D D A N L	S D M H E R T M E	G Y I T K	827
		D I L D G G G D D	D V L L H G G A G N D	I Y F R K G D G N	D T I Y D G D T G . N	D K L S A F A D D A N L	S D M H E R T M E	G Y I T K	830
									893
MbxA	LkxA	R I D	H S G S I N T P R M	T I	Q N Y Q S N K T D H	K I K E Q	S Y T R T S D Q H D K	T L Q D K	859
ApixIIA	HlyA	T I Q	K M P S I N T P R M	T I	P N Y K A K N . D E	K I K E Q	S Y T R T S D Q H D K	T L Q D K	882
		K A E G N V L S I G	H K N G I F Y F K N	T I	S N	K I K E Q	S Y T R T S D Q H D K	T L Q D K	885
									949
MbxA	LkxA	R D G T V T S Q G	L K R L A D E N K L	Q L S A S D V T A S	S L N K L T G S H A	L F G F F A N S S V S S	N A N Q P I T Q V F	Q G I H A	924
ApixIIA	HlyA	R D G T V T S Q G	L K R L A D E N K L	Q L S A S D V T A S	S L N K L T G S H A	L F G F F A N S S V S S	N A N Q P I T Q V F	Q G I H A	941
									945
									1011
MbxA	LkxA	P S V	--	927					
ApixIIA	HlyA	Q S L S G T A A A	--	953					
		V S	--	956					
		Y G R N S T I T A	SA	1023					

FIG. 5

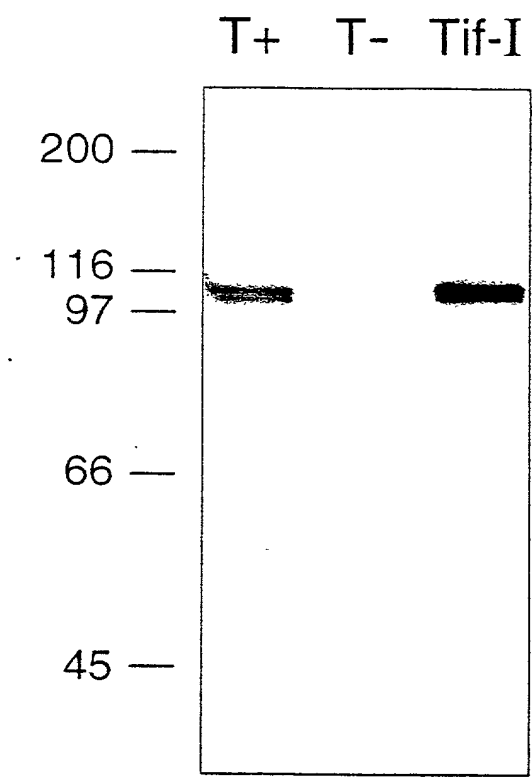


FIG. 6

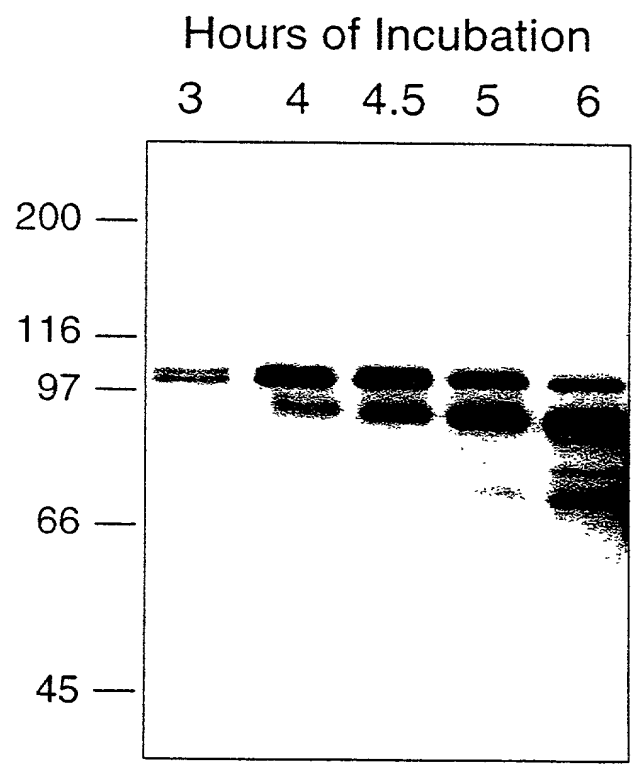
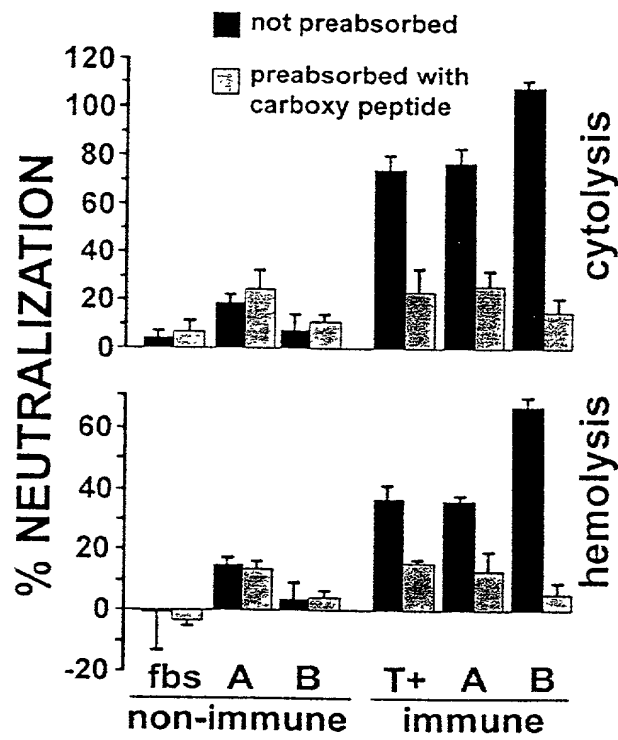


FIG. 7



DNASIS TRANSLATION EDITOR [11-00 B gene.dna]

1 ATGGGTGGTGATACTTCTTTAATTAGACTTAATTTACAAACCTTAATAGTAATTTAGTT 60
 1 M G G D T S L I R N L Q T L N S N L V

61 ATGATAGATTATGCTCAACAACCTGCTCTATCTGCTCTGGTTATCCTTGCCAAATACTAT 120
 21 M I D Y A Q Q P A L S A L V I L A K Y Y 40

121 GGTATTTCTGCAAGTCCAGCAGACATTATGCATCAGTTTTCTGATAATACAAAAGGAGAC 180
 41 G I S A S P A D I M H Q F S D N T K G D 60

181 CTGAATGAAATTGAATGGATGTTGGCAGCAAAGAAATTAGAATTAAGGTAAAGATTATA 240
 61 L N E I E W M L A A K K L E L K V K I I 80

241 AAACAGCCTTTAACTCGATTGTCAATGATAACACTTCCTGCTTTGGTGTGGTGTGATAAT 300
 81 K Q P L T R L S M I T L P A L V W C D N 100

301 AAGCCCGATTAGATCAAAATTTAACTCTCATTTTATACTAACTAAAATTGATGGGGTG 360
 101 K P D L D Q N L N S H F I L T K I D G V 120

361 GGATCTGCTGCAAAATATCTCATCTACGATTTGATTGAGAATCGTCCATAATATTAGAT 420
 121 G S A A K Y L I Y D L I E N R P I I L D 140

421 GCAAGTGAGTTTTCTGAAAGATATTCTGGTAAGTTAATGCTAGTAACTTCCCGTGCGTCA 480
 141 A S E F S E R Y S G K L M L V T S R A S 160

481 ATATTGGGTTTCATTGGCTAAATTTGATTTTACTTGGTTTATTCTGCGGTAATCAAATAT 540
 161 I L G S L A K F D F T W F I P A V I K Y 180

541 CGTTATATTTTTTTGAAGTCATCGTTATTTCAAGTGGTGCTACAGATTTTTGCTCTGATT 600
 181 R Y I F F E V I V I S V V L Q I F A L I 200

601 ACGCCATTGTTTTTTCAGGTTGTGATGGATAAGGTATTGGTGCATCGTGGTTTTTCTACT 660
 201 T P L F F Q V V M D K V L V H R G F S T 220

661 CTGGATGTGGTAGCGATTGCCCTTGTGGTAGTAAGTTTATTTGAAGTCATTTTAAGTGGT 720
 221 L D V V A I A L L V V S L F E V I L S G 240

721 CTACGCACTTATATTTTTGCTCATACAACCTCTCGAATTGATGTAGAGCTAGGAGCACGA 780
 241 L R T Y I F A H T T S R I D V E L G A R 260

781 TTATTTGTCATCTATTAGCTCTACCGCTTGCTTATTTTGAGAGTAGAAGAGTAGGCGAT 840
 261 L F R H L L A L P L A Y F E S R R V G D 280

841 ACAGTTGCACGTATACGTGAATTGGAACATATCCGCAATTTCTTAAGTGGTCAAGCTCTC 900
 281 T V A R I R E L E H I R N F L T G Q A L 300

901 ACTTCAGTTTTAGATTTGGTGTCTTTTATATTCTTGTTTGAATGTGGTATTACAGC 960
 301 T S V L D L V F S F I F L F V M W Y Y S 320

961 CCTACTTTAACAAGTGGTAGTTTTGGCATCATTACCAATATATGCGTTTTGGTCTGCCTTT 1020
 321 P T L T L V V L A S L P I Y A F W S A F 340

1021 ATTAGCCCAATTTTACGCACTCGACTAAATGATCAATTTGCACGCAATGCAGATAATCAA 1080
 341 I S P I L R T R L N D Q F A R N A D N Q 360

1081 TCTTTTTTAGTGGAAGTATTACTGCGGTTGGTACGGTAAAAGCAATGGCAGTTGAACCT 1140
 361 S F L V E S I T A V G T V K A M A V E P 380

1141 CAAATGACCCGTCGCTGGGATAATCAATTAGCAGCTTATGTGGTTTCTAGTTTTCGGGTA 1200
 381 Q M T R R W D N Q L A A Y V V S S F R V 400

1201 GCTAAGTTGGCAATGGTTGGGCAGCAAGGAGTACAACCTATTCAAAGATGGTTATTGTG 1260
 401 A K L A M V G Q Q G V Q L I Q K M V I V 420

1261 GCAACTCTATGGATTGGTGCAAAATTTGGTAATTGAAGGCAAGCTATCGGTAGGTCAATTA 1320
 421 A T L W I G A K L V I E G K L S V G Q L 440

8-1
 mbx
 mbx

09384696 "100501"

DNASIS TRANSLATION EDITOR (11-00) 3 gene.dna3

1321 ATAGCATTTAATATGCTGGCAGGTGAGGTGGCCGCTCCTGTTATCCGCCTGGCACAGCTA	1380
441 I A F N M L A G Q A A P V I R L A Q L	
1381 TGGCAAGATTTTCAGCAAGTAGGTATTTTCAGTGGCGAGATTGGGTGATATTTAAATACT	1440
461 W Q D F Q Q V G I S V A R L G D I L N T	480
1441 CCAACTGAGCATTCTACATCTCGCTTAACCTTACCTGATATTAAGGGTGATATTACATT	1500
481 P T E H S T S R L T L P D I K G D I T F	500
1501 GAAATGTTGATTTTCGCTACAAAATAGATGGGCATTTAATATTACAGAATTTAAATTTA	1560
501 E N V D F R Y K I D G H L I L Q N L N L	520
1561 CAGATTAACGCTGGAGAGATACTAGGTATCGTAGGACGCTCTGGTTCAGGTAAATCAACA	1620
521 Q I N A G E I L G I V G R S G S G K S T	540
1621 TTGACAAAATTAGTACAGCGTTTATATGTACCAGAAAATGGGCGAATATTAGTTGATGGA	1680
541 L T K L V Q R L Y V P E N G R I L V D G	560
1681 AACGATTTGGCATTAGCTGATCCCGCTTGGCTGCGTCGCCAAGTGGGTGTTGTTTTGCAG	1740
561 N D L A L A D P A W L R R Q V G V V L Q	580
1741 GAAATGTGTTACTCAATCGTAGTATTCGAGATAATATTGCCCTAACTGATACGGGCATG	1800
581 E N V L L N R S I R D N I A L T D T G M	600
1801 TCATTAGAGTTTATTATCCAGGCTGCCAAGATGTCTGGGGCACATGACTTTATTATGGAA	1860
601 S L E F I I Q A A K M S G A H D F I M E	620
1861 TTGCCTGAGGGTTATGATACGATTGTTGGAGAGCAAGGTGCAGGCTTGTCAGGTGGACAA	1920
621 L P E G Y D T I V G E Q G A G L S G G Q	640
1921 CGCCAGCGTATCGCTATTGCGCGTGCTTTAATTACCAATCCGCGTATTTTGATTTTGTAT	1980
641 R Q R I A I A R A L I T N P R I L I F D	660
1981 GAAGCTACTAGTGCATTAGACTATGAGTCGGAAAGGGCTATTATGCAAAATATGCAGGCA	2040
661 E A T S A L D Y E S E R A I M Q N M Q A	680
2041 ATTTGCCAAGGTAGAACAGTGTGATTATTGCACATCGCTTATCTACCGTAAAAATGGCA	2100
681 I C Q G R T V L I I A H R L S T V K M A	700
2101 CATCGCATTATTGCAATGGACAAGGGGAAATTTGTAGAGCAAGGCACACATCAAGAATTG	2160
701 H R I I A M D K G K I V E Q G T H Q E L	720
2161 TTGCAAAAAGAAGATGGTTACTATCGTTATTTATATGATTTGCAGAATGGATAAA	2215
721 L Q K E D G Y Y R Y L Y D L Q N G *	739

716.8-2

09884696 "10501"

F15.9

MbxB	---	M	D	Y	A	Q	P	A	S	A	L	V	I	L	A	N	T	G	I	S	A	S	P	A	T	M	R	O	F	S	D	N	T	G	D	N	E	I	E	W	L	A	A	K	K	L	E	L	55														
LkTB	M	A	N	I	Q	R	N	D	L	...	G	L	V	A	L	T	M	L	A	Q	T	H	I	S	L	I	N	P	E	E	I	R	K	F	D	L	D	G	K	G	L	S	D	T	A	W	L	L	A	A	K	S	L	A	L	56							
ApXIB	M	D	F	Y	R	E	.	E	D	Y	...	G	L	V	A	L	T	M	L	A	Q	T	H	I	S	L	I	N	P	E	E	I	R	K	F	D	L	D	G	K	G	L	S	D	T	A	W	L	L	A	A	K	S	L	A	L	55						
HlyB	M	D	S	C	K	.	I	D	Y	...	G	L	V	A	L	T	M	L	A	Q	T	H	I	S	L	I	N	P	E	E	I	R	K	F	D	T	D	G	T	G	L	G	L	S	W	L	L	A	A	K	S	L	E	L	55								
MbxB	K	V	I	I	R	O	P	...	T	R	S	M	T	G	A	L	V	M	C	D	N	K	P	D	L	D	Q	N	L	N	S	H	F	L	T	K	I	D	G	V	G	S	A	K	Y	L	L	Y	D	L	I	-	N	R	F	116							
LkTB	K	A	R	H	I	L	A	S	H	S	T	H	L	H	S	A	L	V	M	C	D	N	K	P	D	L	D	Q	N	L	N	S	H	F	L	T	K	I	D	G	V	G	T	-	N	R	F	L	L	Y	N	L	E	Q	D	A	F	107					
ApXIB	K	A	R	H	I	L	A	S	H	S	T	H	L	H	S	A	L	V	M	C	D	N	K	P	D	L	D	Q	N	L	N	S	H	F	L	T	K	I	D	G	V	G	T	-	N	R	F	L	L	Y	N	L	E	Q	D	A	F	106					
HlyB	K	V	I	I	R	O	P	...	T	R	S	M	T	G	A	L	V	M	C	D	N	K	P	D	L	D	Q	N	L	N	S	H	F	L	T	K	I	D	G	V	G	S	A	K	Y	L	L	Y	D	L	I	-	N	R	F	106							
MbxB	I	L	L	A	E	E	F	S	E	R	V	S	G	K	L	M	L	V	T	S	R	A	S	I	L	G	S	L	A	K	P	D	P	T	W	P	I	P	A	V	I	K	R	Y	I	F	F	E	V	-	V	-	S	V	L	Q	I	F	177				
LkTB	Q	I	L	S	T	D	E	F	E	A	C	I	O	G	Q	L	L	L	V	T	S	R	A	S	I	L	G	S	L	A	K	P	D	P	T	W	P	I	P	A	V	I	K	R	K	I	F	E	T	T	I	V	S	I	F	L	Q	I	F	168			
ApXIB	R	I	L	E	Q	A	E	F	E	A	S	L	O	G	K	L	L	L	V	T	S	R	A	S	I	L	G	S	L	A	K	P	D	P	T	W	P	I	P	A	V	I	K	R	K	I	F	E	T	T	I	V	S	I	F	L	Q	I	F	167			
HlyB	R	I	L	E	Q	A	E	F	E	A	S	L	O	G	K	L	L	L	V	T	S	R	A	S	I	L	G	S	L	A	K	P	D	P	T	W	P	I	P	A	V	I	K	R	K	I	F	E	T	T	I	V	S	I	F	L	Q	I	F	167			
MbxB	A	L	I	T	P	L	F	F	Q	V	V	M	D	R	V	L	V	H	R	G	F	S	T	L	D	V	-	A	A	T	L	V	V	S	M	F	E	-	L	S	G	L	R	T	I	F	A	R	S	T	S	A	I	D	V	E	L	G	238				
LkTB	A	L	I	T	P	L	F	F	Q	V	V	M	D	R	V	L	V	H	R	G	F	S	T	L	D	V	-	A	A	T	L	V	V	S	M	F	E	-	L	S	G	L	R	T	I	F	A	R	S	T	S	A	I	D	V	E	L	G	229				
ApXIB	A	L	I	T	P	L	F	F	Q	V	V	M	D	R	V	L	V	H	R	G	F	S	T	L	D	V	-	A	A	T	L	V	V	S	M	F	E	-	L	S	G	L	R	T	I	F	A	R	S	T	S	A	I	D	V	E	L	G	228				
HlyB	A	L	I	T	P	L	F	F	Q	V	V	M	D	R	V	L	V	H	R	G	F	S	T	L	D	V	-	A	A	T	L	V	V	S	M	F	E	-	L	S	G	L	R	T	I	F	A	R	S	T	S	A	I	D	V	E	L	G	228				
MbxB	A	R	L	P	R	H	L	L	A	L	P	-	A	Y	F	E	S	R	R	V	G	D	T	V	A	R	-	R	E	L	-	H	I	R	N	F	L	T	G	O	A	L	T	S	V	L	D	L	V	P	S	F	I	F	L	F	V	M	W	X	299		
LkTB	A	K	L	P	R	H	L	L	S	L	P	I	S	T	P	E	N	R	R	V	G	D	T	V	A	R	-	R	E	L	D	O	I	R	N	F	L	T	G	O	A	L	T	S	V	L	D	L	V	P	S	F	I	F	L	F	V	M	W	X	290		
ApXIB	A	K	L	P	R	H	L	L	S	L	P	I	S	T	P	E	N	R	R	V	G	D	T	V	A	R	-	R	E	L	D	O	I	R	N	F	L	T	G	O	A	L	T	S	V	L	D	L	V	P	S	F	I	F	L	F	V	M	W	X	289		
HlyB	A	K	L	P	R	H	L	L	S	L	P	I	S	T	P	E	S	R	R	V	G	D	T	V	A	R	-	R	E	L	D	O	I	R	N	F	L	T	G	O	A	L	T	S	V	L	D	L	V	P	S	F	I	F	L	F	V	M	W	X	289		
MbxB	S	P	T	L	T	L	V	I	L	A	S	L	P	I	A	P	M	S	A	F	I	S	P	I	L	R	T	R	I	N	D	O	F	A	R	H	A	D	N	O	S	F	L	V	E	S	T	A	I	N	M	I	K	A	N	A	V	E	P	360			
LkTB	S	P	K	L	T	L	V	I	L	L	G	S	L	P	C	M	I	L	W	S	I	F	I	S	P	I	L	R	R	E	L	D	E	K	P	A	R	G	A	D	N	O	S	F	L	V	E	S	T	A	I	N	M	I	K	A	N	A	V	E	P	351	
ApXIB	S	P	K	L	T	L	V	I	L	L	G	S	L	P	C	M	I	L	W	S	I	F	I	S	P	I	L	R	R	E	L	D	E	K	P	A	R	G	A	D	N	O	S	F	L	V	E	S	T	A	I	N	M	I	K	A	N	A	V	E	P	350	
HlyB	S	P	K	L	T	L	V	I	L	L	F	S	L	P	C	T	A	A	M	S	I	F	I	S	P	I	L	R	R	E	L	D	E	K	P	A	R	G	A	D	N	O	S	F	L	V	E	S	T	A	I	N	M	I	K	A	N	A	V	E	P	350	
MbxB	Q	M	T	R	R	W	D	N	O	L	A	S	T	V	S	S	F	R	V	A	K	L	A	M	-	G	Q	O	G	V	O	L	I	O	K	M	V	I	V	A	T	L	W	-	G	A	K	L	V	I	E	G	K	L	S	G	O	L	L	421			
LkTB	Q	M	T	D	T	W	D	K	O	L	A	S	T	V	S	S	F	R	V	T	V	L	A	T	I	G	Q	O	G	V	O	L	I	O	K	M	V	M	V	I	N	L	W	L	-	G	A	R	L	V	I	S	G	D	L	S	I	G	O	L	L	412	
ApXIB	Q	M	T	E	T	W	D	K	O	L	A	S	T	V	S	A	G	F	R	V	T	L	A	T	I	G	Q	O	G	V	O	L	I	O	K	M	V	M	V	I	T	L	W	L	-	G	A	R	L	V	I	S	G	D	L	S	I	G	O	L	L	411	
HlyB	Q	M	T	N	I	W	D	K	O	L	A	G	T	V	A	A	G	F	-	V	T	V	L	A	T	I	G	Q	O	G	-	O	L	I	O	K	M	V	M	-	I	N	L	W	L	-	G	A	R	L	V	I	S	G	D	L	S	I	G	O	L	L	411
MbxB	A	F	N	M	L	A	G	O	V	A	A	P	V	I	R	L	A	Q	L	W	Q	D	F	Q	O	V	G	I	S	V	A	R	L	G	D	-	L	N	T	P	T	E	R	S	T	S	-	L	T	L	P	-	I	K	G	D	I	T	F	R	N	482	
LkTB	A	F	N	M	L	S	G	O	V	A	A	P	V	I	R	L	A	Q	L	W	Q	D	F	Q	O	V	G	I	S	V	T	R	L	G	D	V	-	L	N	S	P	T	E	R	S	T	S	-	L	T	L	P	-	I	K	G	D	I	T	F	R	N	473
ApXIB	A	F	N	M	L	S	G	O	V	A	A	P	V	I	R	L	A	Q	L	W	Q	D	F	Q	O	V	G	I	S	V	T	R	L	G	D	V	-	L	N	S	P	T	E	R	S	T	S	-	L	T	L	P	-	I	K	G	D	I	T	F	R	N	472
HlyB	A	F	N	M	L	A	G	O	V	A	A	P	V	I	R	L	A	Q	L	W	Q	D	F	Q	O	V	G	I	S	V	T	R	L	G	D	V	-	L	N	S	P	T	E	R	S	T	S	-	L	T	L	P	-	I	K	G	D	I	T	F	R	N	472
MbxB	I	R	F	R	I	K	P	D	A	H	L	I	L	O	S	L	N	L	Q	I	N	A	G	E	-	G	I	V	C	R	S	G	S	G	K	-	S	T	L	T	K	L	-	O	R	L	Y	-	P	E	N	G	R	-	T	A	D	G	N	D	L	543	
LkTB	I	R	F	R	I	K	P	D	A	H	L	I	L	O	S	L	N	L	Q	I	N	A	G	E	-	G	I	V	C	R	S	G	S	G	K	-	S	T	L	T	K	L	-	O	R	L	Y	-	P	E	N	G	R	-	T	A	D	G	N	D	L	534	
ApXIB	I	R	F	R	I	K	P	D	A	H	L	I	L	O	S	L	N	L	Q	I	N	A	G	E	-	G	I	V	C	R	S	G	S	G	K	-	S	T	L	T	K	L	-	O	R	L	Y	-	P	E	N	G	R	-	T	A	D	G	N	D	L	533	
HlyB	I	R	F	R	I	K	P	D	S	H	L	I	L	O	S	L	N	L	Q	I	N	A	G	E	-	G	I	V	C	R	S	G	S	G	K	-	S	T	L	T	K	L	-	O	R	L	Y	-	P	E	N	G	R	-	T	A	D	G	N	D	L	533	
MbxB	A	L	A	D	F	A	N	L	E	R	Q	V	G	V	L	Q	-	N	V	L	L	R	S	I	R	-	D	N	I	A	L	T	D	T	G	-	M	S	-	E	F	I	I	Q	A	-	A	K	-	S	G	A	R	D	F	I	M	E	L	P	E	G	604
LkTB	A	L	A	D	F	A	N	L	E	R	Q	V	G	V	L	Q	-	N	V	L	L	R	S	I	R	-	D	N	I	A	L	T	D	T	G	-	M	S	-	E	F	I	I	Q	A	-	A	K	-	S	G	A	R	D	F	I	M	E	L	P	E	G	595
ApXIB	A	L	A	D	F	A	N	L	E	R	Q	V	G	V	L	Q	-	N	V	L	L	R	S	I	R	-	D	N	I	A	L	T	D	T	G	-																											

FIG. 10

DNASIS Translation Editor [11-00 C gene.dna]

1	ATGACGAAAAAGTTTGCAGAGCTAGGTTTAATTGCATGGCTTTGGTCTAACTCTGATATG	60
1	M T K K F A E L G L I A W L W S N S D M	20
61	CATAAACATTGGACGTTGTCTTTGTTTGGCACCAGTATTCCGGCAATTGAGACAGGT	120
21	H K H W T L S L F A T N V I P A I E T G	40
121	CAATATGTTATATTGAAAAGAGAAGATATGCCTGTAGCATATTGTAGTTGGGCTAACTT	180
41	Q Y V I L K R E D M P V A Y C S W A K L	60
181	AGTTTAGAAAACGAGGTTAAATATATTAACGATGTTACTTCTCTTAAGTTAGATGACTGG	240
61	S L E N E V K Y I N D V T S L K L D D W	80
241	CAGTCAGGTGACCGAACTGGTTTATTGACTGGATTGCTCCATTTGGCGATAGTCTTACA	300
81	Q S G D R N W F I D W I A P F G D S L T	100
301	CTCACAAAACACATGAGAACGTTATTTTCAGATGAATTGTTTAGAGCGATTCTGTAGAT	360
101	L T K H M R T L F S D E L F R A I R V D	120
361	GGAAATTCATCGCATGGTAAGATATCTGAATTTTATGGAAAGTCTGTTGATTCAAATTA	420
121	G N S S H G K I S E F Y G K S V D S K L	140
421	GCCTCAAGAATATTTGCACAATATCACGAAGATTTGACGAGCAAATTGTCAACTCAGAAT	480
141	A S R I F A Q Y H E D L T S K L S T Q N	160
481	AATTTTATTATATCTAAAGATAATTAA	507
161	N F I I S K D N *	169

mbx C
Mbx C

FIG. 11

MbxC	- - - M T K K F A E	L G L I A W L W S N	S D H K H W T L S	L F A T N V I P A I	E T G Q Y	42
LktC	- - M N Q S Y F N L	L G N I T W L W M N	S S L H K E W S C E	L L A R N V I P A I	E N E Q Y	43
ApxC	M S K K I N G F E V	L G E V A W L W A S	S P L H R K W P L S	L L A I N V L P A I	E S N Q Y	45
HlyC	- M N R N N P L E V	L G H V S W L W A S	S P L H R N W P V S	L F A I N V L P A I	R A N Q Y	44

MbxC	V L K R D M P V	A Y C S W A K L S L	E N E V K Y I N D V	T S L K L D D W Q S	G D R N W	87
LktC	M L L I D N G I P I	A Y C S W A D L N L	E T E V K Y I K D I	N S L T P E H W Q S	G D R R W	88
ApxC	V L L K R D G F P I	A C S W A N L N L	E N E I K Y L D D V	A S L V A D D W T S	G D R R W	90
HlyC	A L L T R D N Y P V	A Y C S W A N L S L	E N E I K Y L N D V	T S L V A E D W T S	G D R R W	89

MbxC	F I D W I A P F G D	S L T L T K H M E T	L F S D E L F R A I	R V D G N S S . H G	K I S E F	131
LktC	I I D W I A P F G H	S Q L L Y K K M C Q	K A P D M H V R S I	R F Y F R Q K E L G	K I A Y F	133
ApxC	F I D W I A P F G D	S A A L Y K H M R D	N F P N E L F R A I	R V D P D S R . V G	K I S E F	134
HlyC	F I V W I A P F G D	N G A L Y K M M R K	K F P D E L F R A I	R V D P R T H . V G	K I S E F	133

MbxC	A G K S D S K L A	S I F A Q Y H E E	L T S K L S T Q N N	F I I S K D N -	168
LktC	K G G K D K K T A	K R R F D T Y Q E E	L A T A L K N E F N	F I K K - - -	167
ApxC	H G G R I D K K L A	S K I F Q Y H E E	L M S E L K N E Q M	F K F S L V N S	172
HlyC	H G G K I D R Q L A	N K I F K Q Y H E E	L I T E V K N K S D	F N F S L T G -	170

SEQ ID NO: 32
 SEQ ID NO: 33
 SEQ ID NO: 34
 SEQ ID NO: 35

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DNASIS Translation Editor [11-00 D gene.uno]

1 ATGTTTATACAAGCACTTAAAGATTTTTTTTATTCGCTATATAACCGTTTGGCGCAATACA
 1 M F I Q A L K D F I R Y I T V W R N T

61 TGGGCAGTTCGAGACCACTAACCCCTCCTAAGCGTACTAAAGAAGAACTCGCTTTTCTT 120
 21 W A V R D Q L T P P K R T K E E L A F L 40

121 CCTGCACATCTAGAAGCACTGACACACCTGTATCCAGATCTTCTAAGTGGACAGCTAGA 180
 41 P A H L E L T D T P V S R S S K W T A R 60

181 ATAATCATGATATTTGTCCTATTTGCTTTGCTATGGTCTTGGGTGGACAGATTGACATT 240
 61 I I M I F V L F A L L W S W V G Q I D I 80

241 GTTGCTACAGCTTCAGGTAAAATTTCTTCAGGTAGCCGTAGCAAGACTATTCAATCTTTG 300
 81 V A T A S G K I S S G S R S K T I Q S L 100

301 GAAACAGCGATAGTTAAAGCAGTTTATGTACGTGATGGTCAAAATGTTCAACAAGGTGAA 360
 101 E T A I V K A V Y V R D G Q N V Q Q G E 120

361 ATATTAGTAGATTTAGTGGGAATCGGTTCAAGTAGTGATGTTGCTCAGTCCGAGAAAGCC 420
 121 I L V D L V G I G S D S D V A Q S E K A 140

421 CTTGAGCAGCGCAATTATCTAAGCTACGCCTTGAAGCAATTTTATCAGCATTAAATCAC 480
 141 L R A A Q L S K L R L E A I L S A L N H 160

481 CGTATTAATCCTCAGATTGATGTAGCATATGCAAAGTCTTTAAATATTTTCAAGATCGGAA 540
 161 R I N P Q I D V A Y A K S L N I S E S E 180

541 ATTAATGAAGCTCAAACTTTAGCCCCAAATCAATATCAAGCATGGTTAGCACAAGATGAA 600
 181 I N E A Q T L A Q N Q Y Q A W L A Q D E 200

601 CAACTAAAATTAACCTTAAAAGGACATCAAGCAGAATTACAATCTGCTCGATCCCAAGAA 660
 201 Q L K L T L K G H Q A E L Q S A R S Q E 220

661 CAAAAGTTGGTTTCAGTTGGTGAATTGAACATCAAAAGACTGATGATTATCGGAGTCTC 720
 221 Q K L V S V G A I E H Q K T D D Y R S L 240

721 AAAGCAGAAAATTTTATATCTGAGCATGCTTATCTAGAACAAGAAAGCAAATTACTTAGC 780
 241 K A E N F I S E H A Y L E Q E S K L L S 260

781 AATCAAAATGATTTACAAAGTACACGTAGTCAGATTCAAAAAATACAGGCTGCAATCATG 840
 261 N Q N D L Q S T R S Q I Q K I Q A A I M 280

841 CAAGCTGAACAGAACCGTATGTTATATACTCAAAATCTAAAACGTGATACATTAGAATCT 900
 281 Q A E Q N R M L Y T Q N L K R D T L E S 300

901 TTACGCCAAACCAATGAACAGATTAATCAATATACTGGTCAAATAATAAGCTAAGCAG 960
 301 L R Q T N E Q I N Q Y T G Q T N K A K Q 320

961 CGACAGAAAATTGCTGAGTATTAATCACCTGTTAATGGTACTATACAAGAGCTAACAGCT 1020
 321 R Q K L L S I K S P V N G T I Q E L T A 340

1021 TATACTTTAGGTGGAGTTGTACAAGCAGCACAAAAAATTATGGTTGTGGCACCTAACGAT 1080
 341 Y T L G G V V Q A A Q K I M V V A P N D 360

1081 AATCAAGTGAAGTAGAGGTATTAGTGCTAAATAAAGATATCGGCTTTGTAAAAGCTGGG 1140
 361 N Q V E V E V L V L N K D I G F V K A G 380

1141 CAGAATGTTATCATCAAAATCGAGAGTTTTCTTATACACGTTATGGTTATTTAACAGGT 1200
 381 Q N V I I K I E S F P Y T R Y G Y L T G 400

1201 AAAATAAAAAGTATTAGTCATGATGCTATAGAACATCAACATTTAGGTCTAGTGATACT 1260
 401 K I K S I S H D A I E H Q H L G L V Y T 420

1261 GCACTTGTTTCTCTTGATAAAAGCACATTAATATAGATGGAGTAACAATCAACTTAACG 1320
 421 A L V S L D K S T L N I D G V T I N L T 440

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1321 CCAGGAATGAATGTTACTGCTGAAATTAAACAGGTAAACGTCGTGTTTGGATTATATA 1380
441 P G M N V T A E I T G K R R V L D Y I

1381 TTAAGTCCATTGCAGACAAAAGTTGATGAAAGTTTTCGAGAACGCTAA 1428
461 L S P L Q T K V D E S F R E R *

FIG. 12-2

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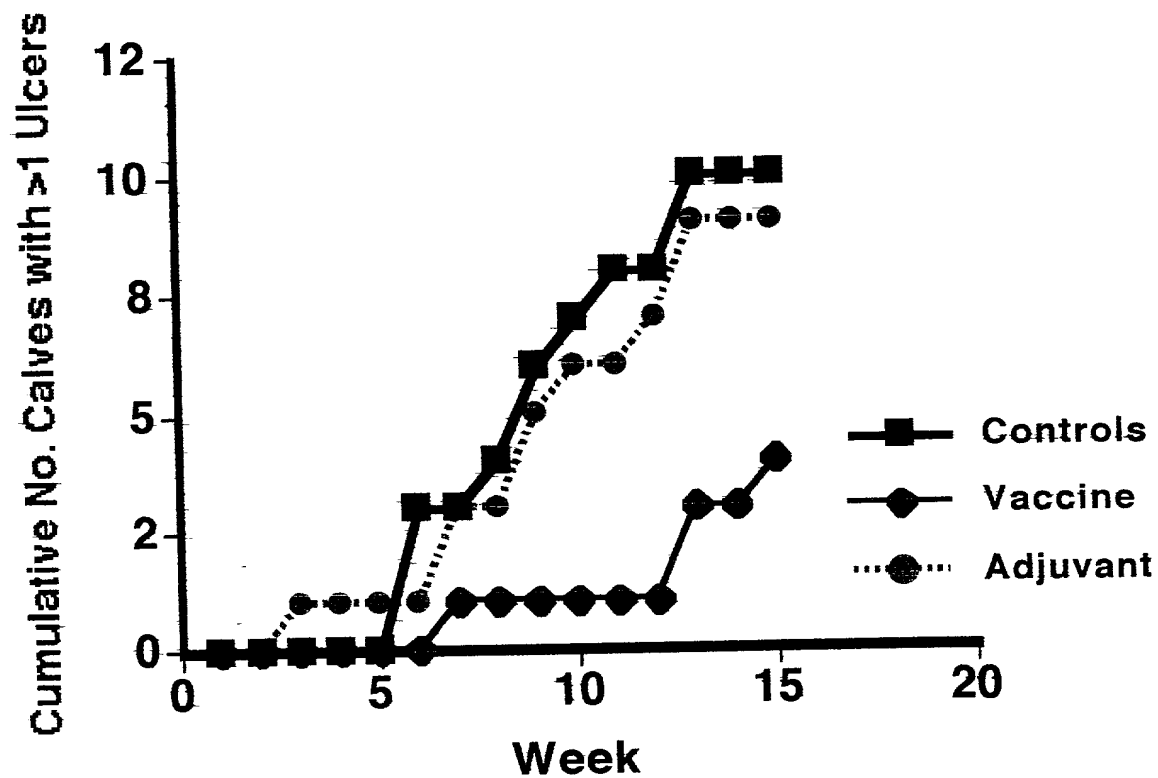
FIG. 13

MbxD	--MF-QALK--	FFRYITVWR	NTWARDOLT	PPKRTKELA	FLPAHLELT	48
Lktd	MKIWLSG YE	FFLRIKN WA	EVWKIRKLD	HPNRKKDESE	FLPAHLELIE	50
ApXID	MKTWLMGLYE	FFQRYKT VWT	EWKIRHOLD	TPDREKDENE	FLPAHLELIE	50
HlyD	MKTWLMGFSE	FLRYKLVWS	ETWKIRKOLD	TPVREKDENE	FLPAHLELIE	50
MbxD	TPVSRSSWT	ARIMFVLF	ALLWSWVGQ	IVATASGK	SSGSRSKTIQ	98
Lktd	TPVSKKPRLI	AYLIMLFLVV	AVLASVSKV	EIVATAPGKL	TFSGRSKEIK	100
ApXID	TPVSKKPRLI	AYLIMLFLFL	ALVSIHV	EIVATATGKL	AFSDRSKEIK	100
HlyD	TPVSRPRLI	AYFIMGFLVI	AFLSVLGQV	EIVATANGKL	TLSGRSKEIK	100
MbxD	S-ETAI VKA	V-DGONV Q	G-LV D LVG	GSDSDVAQSE	KALRAAQLSK	148
Lktd	PIENAI VOEI	FVKDGO FVER	GOLLVSLTAL	GSDADI KKT M	ASLSLAKLEN	150
ApXID	PIENAI VKEI	FVQDGO FVER	DOLLHLTAL	GADADQ QKT K	SSLSLAKLER	150
HlyD	PIENSIVKEI	TVKGSVRK	GDVLLKLTAL	CAADTLKTQ	SSLLQA LEQ	150
MbxD	LRLEA LSA	NHRINPQIDV	AYAKSLNIS	ESEINEAQT L	AQNOYQAWLA	197
Lktd	YRYQTLLTAI	EKESLPVIDL	.SRTEFKDSS	EEDRLRIKHL	IEEQYTTWQK	199
ApXID	YRYETLLLEA	AADRPLLI	.TKDEFKHAT	EEDKTRIRYL	ITEQFEAWQK	199
HlyD	TRYQILSRST	SLNKLPEKL	PDEPYFQNV	EEEVLR TSL	IKQFSTWQK	200
MbxD	QDEQLKLT LK	GHAE LQSAR	SQEQRLVSVG	AIEHKTDD	RSLKAENFIS	247
Lktd	OKTOKT LAYK	RKEABKOTIF	AYRRYEGAT	RIEQEK LKDF	KALYKQKS	249
ApXID	OKYQKELALQ	RBAEKOT L	ANIRKYEG S	RVENERL KDL	KKLFNSKSTS	249
HlyD	OKYQKELNLD	KRAE LTTL	ARIN YENV	RVEKSR LDDF	RSL LHKQAIA	250
MbxD	EHAYLEQESK	LSNQN LQS	TRSQOKIWA	AIQAE NRM	LYTONLKRDT	297
Lktd	KHEL LAQENK	LIEAQN AVAV	YRSKLINE EN	DL LN VKEELE	LITQF FKS D	299
ApXID	KHDVLTQEN	HIEAVWELAV	YKSRLNE ES	DLRQAKEEIH	LITQLF ADI	299
HlyD	KHAVLEQENK	YEAANELRV	YKSQLE IES	ILSAKEEYQ	L TQLFKN I	300
MbxD	LES LR OTNEQ	INOYTG TTNK	AKOROKLLSI	SPVNGT Q	LTA T LGGVV	347
Lktd	LEKLKQH IEN	ERQRLLELER	NNORROASMI	RAPVSGTVQQ	LKIHT IGGVV	349
ApXID	LEKLKQNV EA	EKQLSLELER	NEORQASVI	RAPVSGTVQQ	LKTHTVGGVV	349
HlyD	LKLROTT S	IELLTLELER	NE RQASVI	RAPVSGKVQQ	LKVHTEGGVV	350
MbxD	QAATK MVIA	PNDNQVEVEV	LVLNKDIGFV	KAGQNV IIKV	ESFFPYTRYGY	397
Lktd	TTAETLM IV	PEDDVLEATA	LVPNKDIGFV	AAGQEV IIKV	ETFPYTRYGY	399
ApXID	TTAETLMVIA	PEDDVLEVTA	LQNKDIGFI	EVGQDA IKV	ETFPYTRYGY	399
HlyD	TTAETLMVIV	PEDDTLEVTA	LQNKDIGFI	NVGQNA IIKV	EAPPYTRYGY	400
MbxD	LTGKIKSISH	DAIEHQHLGL	VTAZVSDD	STLN IDGVT	INLT PGMNVT	446
Lktd	LTGKIKHISP	DAIEQPNVGL	VFNATIAIDR	KNLTSPDG K	IDLSSGMT T	449
ApXID	LMGKVKNTL	DAIEHPQLGL	VFNSTIISIDR	KTLSGKDGKE	IELGSGMSVT	449
HlyD	LVGKVKNTL	DAIEDQKLGL	VFNSTIISIDR	NDLST GNRH	IPLSSGMAVT	449
MbxD	AEIKTGKRRV	EDYLSPLRT	KVDESFRER	475	SEQ ID NO: 37	
Lktd	AEIKTGERSV	MSYLLSPLER	SVTESLRER	478	SEQ ID NO: 38	
ApXID	AEIKTGERSV	ISYLLSPLER	SVTESLRER	478	SEQ ID NO: 39	
HlyD	AEIKTGMRSV	ISYLLSPLER	SVTESLRER	478	SEQ ID NO: 40	

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FIG. 14

Cumulative Number of Calves With Severe Ulcers



Number of calves with ulcers with clinical scores >+2

FIG 15

Number of calves affected each week

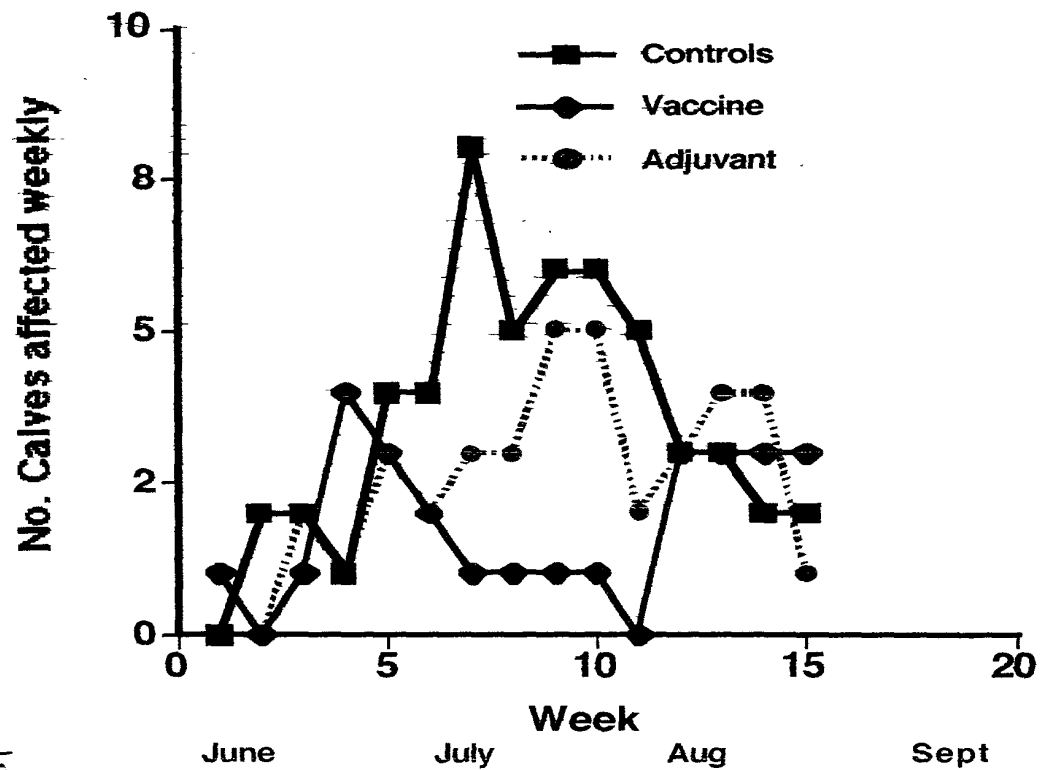
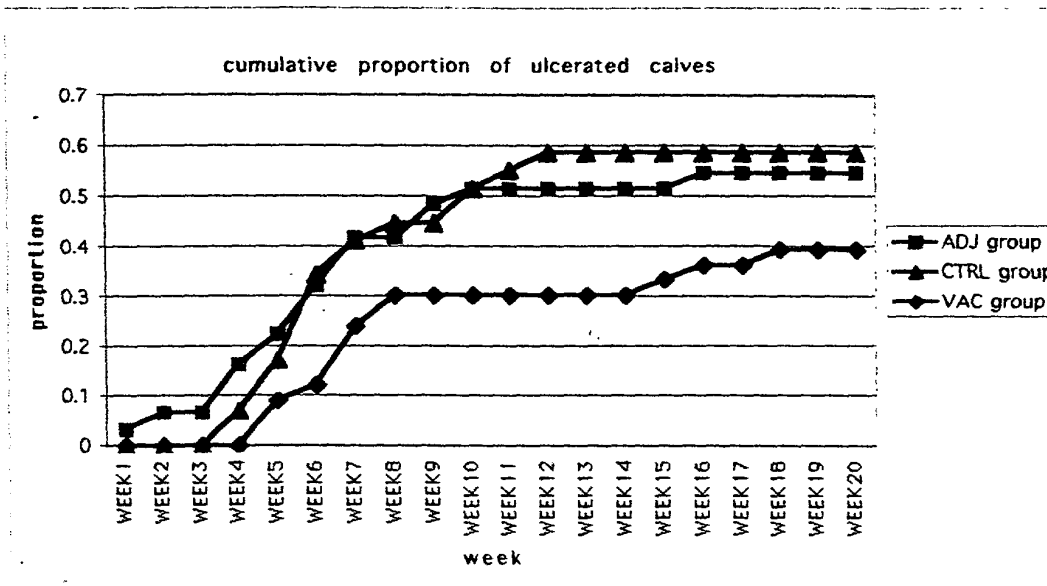


Figure 15
Number of calves affected weekly in 1 group of vaccinated calves and in controls.

FIG. 16



Cumulative proportion of ulcerated calves during the trial. Calves received as vaccines either saline (designated 'CTRL'), adjuvant alone (designated 'ADJ'), or the recombinant cytotoxin vaccine (designated 'VAC').